

CRF Errors Corrected by the STIC Systems Branch

CRF Processing Date: 4/5/02

Edited by: DC

Verified by: DC (STIC staff) cyoy

Serial Number: 10/006,883A

F3

ENTERED

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: _____
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____
- ☒ Deleted: ☒ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted **ending** stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☐ Other: _____

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95



OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/006,883A

DATE: 04/05/2002
TIME: 16:25:00

Input Set : A:\PTO.DC.txt

Output Set: N:\CRF3\04052002\J006883A.raw

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3 <110> APPLICANT: Kenneth W. Dobie
5 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF NOD1 EXPRESSION
7 <130> FILE REFERENCE: RTS-0337
9 <140> CURRENT APPLICATION NUMBER: US/10/006,883A
10 <141> CURRENT FILING DATE: 2001-12-05
12 <160> NUMBER OF SEQ ID NOS: 96
14 <210> SEQ ID NO: 1
15 <211> LENGTH: 20
16 <212> TYPE: DNA
17 <213> ORGANISM: Artificial Sequence
19 <220> FEATURE:
20 <223> OTHER INFORMATION: Antisense Oligonucleotide
22 <400> SEQUENCE: 1
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26 <210> SEQ ID NO: 2
27 <211> LENGTH: 20
28 <212> TYPE: DNA
29 <213> ORGANISM: Artificial Sequence
31 <220> FEATURE:
32 <223> OTHER INFORMATION: Antisense Oligonucleotide
34 <400> SEQUENCE: 2
35 atgcattctg cccccaagga
38 <210> SEQ ID NO: 3
39 <211> LENGTH: 4390
40 <212> TYPE: DNA
41 <213> ORGANISM: Homo sapiens
43 <220> FEATURE:
44 <221> NAME/KEY: CDS
45 <222> LOCATION: (425)...(3286)
47 <400> SEQUENCE: 3
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49 agactttcct tcggtttctg cctttgatgg caatttcctt cggtttctgc ctttgatggc
50 aagagggtgga gattgtggcg gcgattacag agaacgtctg ggaagacaag ttgctgtttt
51 tatgggaatc gcaggcttgg aagagacaga agcaattcca gaaataaatt ggaaattgaa
52 gatttaaaca atgttgtttt aaaatattct aacttcaaag aatgatgcca gaaacttaaa
53 aaggggctgc gcagagtagc aggggcccctg gagggcgcgg cctgaatcct gattgccctt
54 ctgctgagag gacacacgca gctgaagatg aatttgggaa aagtagccgc ttgctacttt
55 aact atg gaa gag cag ggc cac agt gag atg gaa ata atc cca tca gag
56 Met Glu Glu Gln Gly His Ser Glu Met Glu Ile Ile Pro Ser Glu
57 1 5 10 15
58 tct cac ccc cac att caa tta ctg aaa agc aat cgg gaa ctt ctg gtc
59 Ser His Pro His Ile Gln Leu Leu Lys Ser Asn Arg Glu Leu Leu Val
60 20 25 30

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70 act cac atc cgc aat act cag tgt ctg gtg gac aac ttg ctg aag aat      565
71 Thr His Ile Arg Asn Thr Gln Cys Leu Val Asp Asn Leu Leu Lys Asn
72          35          40          45
74 gac tac ttc tcg gcc gaa gat gcg gag att gtg tgt gcc tgc ccc acc      613
75 Asp Tyr Phe Ser Ala Glu Asp Ala Glu Ile Val Cys Ala Cys Pro Thr
76          50          55          60
78 cag cct gac aag gtc cgc aaa att ctg gac ctg gta cag agc aag ggc      661
79 Gln Pro Asp Lys Val Arg Lys Ile Leu Asp Leu Val Gln Ser Lys Gly
80          65          70          75
82 gag gag gtg tcc gag ttc ttc ctc tac ttg ctc cag caa ctc gca gat      709
83 Glu Glu Val Ser Glu Phe Phe Leu Tyr Leu Leu Gln Gln Leu Ala Asp
84 80          85          90          95
86 gcc tac gtg gac ctc agg cct tgg ctg ctg gag atc ggc ttc tcc cct      757
87 Ala Tyr Val Asp Leu Arg Pro Trp Leu Leu Glu Ile Gly Phe Ser Pro
88          100          105          110
90 tcc ctg ctc act cag agc aaa gtc gtg gtc aac act gac cca gtg agc      805
91 Ser Leu Leu Thr Gln Ser Lys Val Val Val Asn Thr Asp Pro Val Ser
92          115          120          125
94 agg tat acc cag cag ctg cga cac cat ctg ggc cgt gac tcc aag ttc      853
95 Arg Tyr Thr Gln Gln Leu Arg His His Leu Gly Arg Asp Ser Lys Phe
96          130          135          140
98 gtg ctg tgc tat gcc cag aag gag gag ctg ctg ctg gag gag atc tac      901
99 Val Leu Cys Tyr Ala Gln Lys Glu Glu Leu Leu Leu Glu Glu Ile Tyr
100          145          150          155
102 atg gac acc atc atg gag ctg gtt ggc ttc agc aat gag agc ctg ggc      949
103 Met Asp Thr Ile Met Glu Leu Val Gly Phe Ser Asn Glu Ser Leu Gly
104 160          165          170          175
106 agc ctg aac agc ctg gcc tgc ctc ctg gac cac acc acc ggc atc ctc      997
107 Ser Leu Asn Ser Leu Ala Cys Leu Leu Asp His Thr Thr Gly Ile Leu
108          180          185          190
110 aat gag cag ggt gag acc atc ttc atc ctg ggt gat gct ggg gtg ggc      1045
111 Asn Glu Gln Gly Glu Thr Ile Phe Ile Leu Gly Asp Ala Gly Val Gly
112          195          200          205
114 aag tcc atg ctg cta cag cgg ctg cag agc ctc tgg gcc acg ggc cgg      1093
115 Lys Ser Met Leu Leu Gln Arg Leu Gln Ser Leu Trp Ala Thr Gly Arg
116          210          215          220
118 cta gac gca ggg gtc aaa ttc ttc ttc cac ttt cgc tgc cgc atg ttc      1141
119 Leu Asp Ala Gly Val Lys Phe Phe Phe His Phe Arg Cys Arg Met Phe
120          225          230          235
122 agc tgc ttc aag gaa agt gac agg ctg tgt ctg cag gac ctg ctc ttc      1189
123 Ser Cys Phe Lys Glu Ser Asp Arg Leu Cys Leu Gln Asp Leu Leu Phe
124 240          245          250          255
126 aag cac tac tgc tac cca gag cgg gac ccc gag gag gtg ttt gcc ttc      1237
127 Lys His Tyr Cys Tyr Pro Glu Arg Asp Pro Glu Glu Val Phe Ala Phe
128          260          265          270
130 ctg ctg cgc ttc ccc cac gtg gcc ctc ttc acc ttc gat ggc ctg gac      1285
131 Leu Leu Arg Phe Pro His Val Ala Leu Phe Thr Phe Asp Gly Leu Asp
132          275          280          285
134 gag ctg cac tcg gac ttg gac ctg agc cgc gtg cct gac agc tcc tgc      1333

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135	Glu	Leu	His	Ser	Asp	Leu	Asp	Leu	Ser	Arg	Val	Pro	Asp	Ser	Ser	Cys	
136			290					295					300				
138	ccc	tgg	gag	cct	gcc	cac	ccc	ctg	gtc	ttg	ctg	gcc	aac	ctg	ctc	agt	1381
139	Pro	Trp	Glu	Pro	Ala	His	Pro	Leu	Val	Leu	Leu	Ala	Asn	Leu	Leu	Ser	
140		305					310					315					
142	ggg	aag	ctg	ctc	aag	ggg	gct	agc	aag	ctg	ctc	aca	gcc	cgc	aca	ggc	1429
143	Gly	Lys	Leu	Leu	Lys	Gly	Ala	Ser	Lys	Leu	Leu	Thr	Ala	Arg	Thr	Gly	
144	320					325					330					335	
146	atc	gag	gtc	ccg	cgc	cag	ttc	ctg	cgg	aag	aag	gtg	ctt	ctc	cgg	ggc	1477
147	Ile	Glu	Val	Pro	Arg	Gln	Phe	Leu	Arg	Lys	Lys	Val	Leu	Leu	Arg	Gly	
148					340				345						350		
150	ttc	tcc	ccc	agc	cac	ctg	cgc	gcc	tat	gcc	agg	agg	atg	ttc	ccc	gag	1525
151	Phe	Ser	Pro	Ser	His	Leu	Arg	Ala	Tyr	Ala	Arg	Arg	Met	Phe	Pro	Glu	
152				355					360					365			
154	cgg	gcc	ctg	cag	gac	cgc	ctg	ctg	agc	cag	ctg	gag	gcc	aac	ccc	aac	1573
155	Arg	Ala	Leu	Gln	Asp	Arg	Leu	Leu	Ser	Gln	Leu	Glu	Ala	Asn	Pro	Asn	
156			370					375					380				
158	ctc	tgc	agc	ctg	tgc	tct	gtg	ccc	ctc	ttc	tgc	tgg	atc	atc	ttc	cgg	1621
159	Leu	Cys	Ser	Leu	Cys	Ser	Val	Pro	Leu	Phe	Cys	Trp	Ile	Ile	Phe	Arg	
160		385				390					395						
162	tgc	ttc	cag	cac	ttc	cgt	gct	gcc	ttt	gaa	ggc	tca	cca	cag	ctg	ccc	1669
163	Cys	Phe	Gln	His	Phe	Arg	Ala	Ala	Phe	Glu	Gly	Ser	Pro	Gln	Leu	Pro	
164	400				405					410						415	
166	gac	tgc	acg	atg	acc	ctg	aca	gat	gtc	ttc	ctc	ctg	gtc	act	gag	gtc	1717
167	Asp	Cys	Thr	Met	Thr	Leu	Thr	Asp	Val	Phe	Leu	Leu	Val	Thr	Glu	Val	
168				420					425						430		
170	cat	ctg	aac	agg	atg	cag	ccc	agc	agc	ctg	gtg	cag	cgg	aac	aca	cgc	1765
171	His	Leu	Asn	Arg	Met	Gln	Pro	Ser	Ser	Leu	Val	Gln	Arg	Asn	Thr	Arg	
172			435					440					445				
174	agc	cca	gtg	gag	acc	ctc	cac	gcc	ggc	cgg	gac	act	ctg	tgc	tgc	ctg	1813
175	Ser	Pro	Val	Glu	Thr	Leu	His	Ala	Gly	Arg	Asp	Thr	Leu	Cys	Ser	Leu	
176			450					455				460					
178	ggg	cag	gtg	gcc	cac	cgg	ggc	atg	gag	aag	agc	ctc	ttt	gtc	ttc	acc	1861
179	Gly	Gln	Val	Ala	His	Arg	Gly	Met	Glu	Lys	Ser	Leu	Phe	Val	Phe	Thr	
180		465				470					475						
182	cag	gag	gag	gtg	cag	gcc	tcc	ggg	ctg	cag	gag	aga	gac	atg	cag	ctg	1909
183	Gln	Glu	Glu	Val	Gln	Ala	Ser	Gly	Leu	Gln	Glu	Arg	Asp	Met	Gln	Leu	
184	480				485					490					495		
186	ggc	ttc	ctg	cgg	gct	ttg	ccg	gag	ctg	ggc	ccc	ggg	ggt	gac	cag	cag	1957
187	Gly	Phe	Leu	Arg	Ala	Leu	Pro	Glu	Leu	Gly	Pro	Gly	Gly	Asp	Gln	Gln	
188				500					505				510				
190	tcc	tat	gag	ttt	ttc	cac	ctc	acc	ctc	cag	gcc	ttc	ttt	aca	gcc	ttc	2005
191	Ser	Tyr	Glu	Phe	Phe	His	Leu	Thr	Leu	Gln	Ala	Phe	Phe	Thr	Ala	Phe	
192			515					520				525					
194	ttc	ctc	gtg	ctg	gac	gac	agg	gtg	ggc	act	cag	gag	ctg	ctc	agg	ttc	2053
195	Phe	Leu	Val	Leu	Asp	Asp	Arg	Val	Gly	Thr	Gln	Glu	Leu	Leu	Arg	Phe	
196			530					535				540					
198	ttc	cag	gag	tgg	atg	ccc	cct	gcg	ggg	gca	gcg	acc	acg	tcc	tgc	tat	2101
199	Phe	Gln	Glu	Trp	Met	Pro	Pro	Ala	Gly	Ala	Ala	Thr	Thr	Ser	Cys	Tyr	

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Input Set : A:\PTO.DC.txt

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200	545	550	555	
202	cct ccc ttc ctc ccg ttc	cag tgc ctg cag ggc agt ggt ccg gcg cgg	2149	
203	Pro Pro Phe Leu Pro Phe	Gln Cys Leu Gln Gly Ser Gly Pro Ala Arg		
204	560	565	570	575
206	gaa gac ctc ttc aag aac aag gat cac ttc	cag ttc acc aac ctc ttc	2197	
207	Glu Asp Leu Phe Lys Asn Lys Asp His	Phe Gln Phe Thr Asn Leu Phe		
208	580	585	590	
210	ctg tgc ggg ctg ttg tcc aaa gcc aaa cag aaa ctc	ctg cgg cat ctg	2245	
211	Leu Cys Gly Leu Leu Ser Lys Ala Lys Gln Lys Leu Leu Arg His Leu			
212	595	600	605	
214	gtg ccc gcg gca gcc ctg agg aga aag cgc aag gcc	ctg tgg gca cac	2293	
215	Val Pro Ala Ala Ala Leu Arg Arg Lys Arg Lys Ala Leu Trp Ala His			
216	610	615	620	
218	ctg ttt tcc agc ctg cgg ggc tac ctg aag agc	ctg ccc cgc gtt cag	2341	
219	Leu Phe Ser Ser Leu Arg Gly Tyr Leu Lys Ser Leu Pro Arg Val Gln			
220	625	630	635	
222	gtc gaa agc ttc aac cag gtg cag gcc atg ccc acg ttc atc tgg atg		2389	
223	Val Glu Ser Phe Asn Gln Val Gln Ala Met Pro Thr Phe Ile Trp Met			
224	640	645	650	655
226	ctg cgc tgc atc tac gag aca cag agc cag aag gtg ggg cag ctg gcg		2437	
227	Leu Arg Cys Ile Tyr Glu Thr Gln Ser Gln Lys Val Gly Gln Leu Ala			
228	660	665	670	
230	gcc agg ggc atc tgc gcc aac tac ctc aag ctg acc tac tgc aac gcc		2485	
231	Ala Arg Gly Ile Cys Ala Asn Tyr Leu Lys Leu Thr Tyr Cys Asn Ala			
232	675	680	685	
234	tgc tcg gcc gac tgc agc gcc ctc tcc ttc gtc ctg cat cac ttc ccc		2533	
235	Cys Ser Ala Asp Cys Ser Ala Leu Ser Phe Val Leu His His Phe Pro			
236	690	695	700	
238	aag cgg ctg gcc cta gac cta gac aac aac aat ctc aac gac tac ggc		2581	
239	Lys Arg Leu Ala Leu Asp Leu Asp Asn Asn Asn Leu Asn Asp Tyr Gly			
240	705	710	715	
242	gtg cgg gag ctg cag ccc tgc ttc agc cgc ctc act gtt ctc aga ctc		2629	
243	Val Arg Glu Leu Gln Pro Cys Phe Ser Arg Leu Thr Val Leu Arg Leu			
244	720	725	730	735
246	agc gta aac cag atc act gac ggt ggg gta aag gtg cta agc gaa gag		2677	
247	Ser Val Asn Gln Ile Thr Asp Gly Gly Val Lys Val Leu Ser Glu Glu			
248	740	745	750	
250	ctg acc aaa tac aaa att gtg acc tat ttg ggt tta tac aac aac cag		2725	
251	Leu Thr Lys Tyr Lys Ile Val Thr Tyr Leu Gly Leu Tyr Asn Asn Gln			
252	755	760	765	
254	atc acc gat gtc gga gcc agg tac gtc acc aaa atc ctg gat gaa tgc		2773	
255	Ile Thr Asp Val Gly Ala Arg Tyr Val Thr Lys Ile Leu Asp Glu Cys			
256	770	775	780	
258	aaa ggc ctc acg cat ctt aaa ctg gga aaa aac aaa ata aca agt gaa		2821	
259	Lys Gly Leu Thr His Leu Lys Leu Gly Lys Asn Lys Ile Thr Ser Glu			
260	785	790	795	
262	gga ggg aag tat ctc gcc ctg gct gtg aag aac agc aaa tca atc tct		2869	
263	Gly Gly Lys Tyr Leu Ala Leu Ala Val Lys Asn Ser Lys Ser Ile Ser			
264	800	805	810	815

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266 gag gtt ggg atg tgg ggc aat caa gtt ggg gat gaa gga gca aaa gcc 2917
267 Glu Val Gly Met Trp Gly Asn Gln Val Gly Asp Glu Gly Ala Lys Ala
268      820      825      830
270 ttc gca gag gct ctg cgg aac cac ccc agc ttg acc acc ctg agt ctt 2965
271 Phe Ala Glu Ala Leu Arg Asn His Pro Ser Leu Thr Thr Leu Ser Leu
272      835      840      845
274 gcg tcc aac ggc atc tcc aca gaa gga gga aag agc ctt gcg agg gcc 3013
275 Ala Ser Asn Gly Ile Ser Thr Glu Gly Gly Lys Ser Leu Ala Arg Ala
276      850      855      860
278 ctg cag cag aac acg tct cta gaa ata ctg tgg ctg acc caa aat gaa 3061
279 Leu Gln Gln Asn Thr Ser Leu Glu Ile Leu Trp Leu Thr Gln Asn Glu
280      865      870      875
282 ctc aac gat gaa gtg gca gag agt ttg gca gaa atg ttg aaa gtc aac 3109
283 Leu Asn Asp Glu Val Ala Glu Ser Leu Ala Glu Met Leu Lys Val Asn
284 880      885      890      895
286 cag acg tta aag cat tta tgg ctt atc cag aat cag atc aca gct aag 3157
287 Gln Thr Leu Lys His Leu Trp Leu Ile Gln Asn Gln Ile Thr Ala Lys
288      900      905      910
290 ggg act gcc cag ctg gca gat gcg tta cag agc aac act ggc ata aca 3205
291 Gly Thr Ala Gln Leu Ala Asp Ala Leu Gln Ser Asn Thr Gly Ile Thr
292      915      920      925
294 gag att tgc cta aat gga aac ctg ata aaa cca gag gag gcc aaa gtc 3253
295 Glu Ile Cys Leu Asn Gly Asn Leu Ile Lys Pro Glu Glu Ala Lys Val
296      930      935      940
298 tat gaa gat gag aag cgg att atc tgt ttc tga gaggatgctt tcctgttcat 3306
299 Tyr Glu Asp Glu Lys Arg Ile Ile Cys Phe
300      945      950
302 ggggtttttt ccctggagcc tcagcagcaa atgccactct gggcagtctt ttgtgtcagt 3366
304 gtcttaaagg ggcctgcgca ggcgggacta tcaggagtcc actgcctcca tgatgcaagc 3426
306 cagcttcctg tgcagaaggt ctggtcggca aactccctaa gtaccgcta caattctgca 3486
308 gaaaaagaat gtgtcttgcg agctgttgta gttacagtaa atacactgtg aagagacttt 3546
310 attgcctatt ataattattt ttatctgaag ctagaggaat aaagctgtga gcaaacagag 3606
312 gagggcagcc tcacctcatt ccaacacctg ccatagggac caacgggagc gagttgggtca 3666
314 ccgctctttt cattgaagag ttgaggatgt ggcacaaagt tgggtgccaag cttcttgaat 3726
316 aaaacgtggt tgatggatta gtattatacc tgaaatattt tcttccttct cagcactttc 3786
318 ccatgtattg atactgggtc cacttcacag ctggagacac cggagtatgt gcagtgtggg 3846
320 atttgactcc tccaagggtt tgtggaaagt taatgtcaag gaaaggatgc accacgggct 3906
322 tttaatttta atcctggagt ctactgtct gctggcaaag atagagaatg ccctcagctc 3966
324 ttagctggtc taagaatgac gatgccttca aaatgctgct tccactcagg gcttctcctc 4026
326 tgctaggcta cctcctctca gaaggctgag taccatgggc tacagtgtct ggccttgga 4086
328 agaagtgatt ctgtccctcc aaagaaatag ggcattggctt gcccctgtgg ccctggcatc 4146
330 caaatggctg cttttgtctc cttacctcg tgaagagggg aagtctcttc ctgcctccca 4206
332 agcagctgaa ggggtgactaa acgggcgcca agactcaggg gatcggtctg gaactgggcc 4266
334 agcagagcat gttggacacc cccaccatg gtgggcttgt ggtggctgct ccatgagggt 4326
336 gggggtgata ctactagatc acttgtcctc ttgcccgctc atttgtaaat aaaatactga 4386
338 aaac 4390
341 <210> SEQ ID NO: 4
342 <211> LENGTH: 19
343 <212> TYPE: DNA

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/006,883A

DATE: 04/05/2002
TIME: 16:25:01

Input Set : A:\PTO.DC.txt
Output Set: N:\CRF3\04052002\J006883A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:12; N Pos. 38
Seq#:12; Xaa Pos. 11
Seq#:14; N Pos. 8
Seq#:15; N Pos. 425,426,427,428,429,430,431,432,433,434,435,436,437,438,439
Seq#:15; N Pos. 440,441,442,443,444,445,446,447,448,449,450,451,452,453,454
Seq#:15; N Pos. 455,456,457,458,459,460,461,462,463,464,465,466,467,468,469
Seq#:15; N Pos. 470,471,472,473,474,475,476,477,478,479,480,481,482,483,484
Seq#:15; N Pos. 485,486,487,488,489,490,491,492,493,494,495,496,497,498,499
Seq#:15; N Pos. 500,501,502,503,504,505,506,507,508,509,510,511,512,513,514
Seq#:15; N Pos. 515,516,517,518,519,520,521,522,523,524
Seq#:95; N Pos. 72
Seq#:96; N Pos. 1394

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/006,883A

DATE: 04/05/2002

TIME: 16:25:01

Input Set : A:\PTO.DC.txt

Output Set: N:\CRF3\04052002\J006883A.raw

L:419 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10
L:1157 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:11
L:1162 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:11
L:1337 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:0
L:1338 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:48
L:1358 M:283 W: Missing Blank Line separator, <400> field identifier
L:1359 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (13) SEQUENCE:
L:1372 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:14
L:1377 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:0
L:1395 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:15
L:1400 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:15
L:1410 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:15
L:1415 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:15
L:1425 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:15
L:1435 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:15
L:1452 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:420
L:1453 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:480
L:3019 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:95 after pos.:60
L:3126 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:96 after pos.:1380